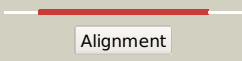



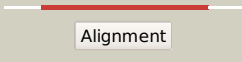




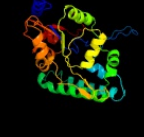
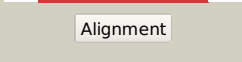

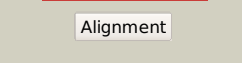

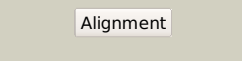

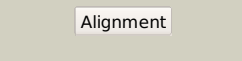

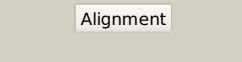

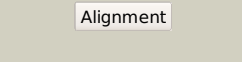






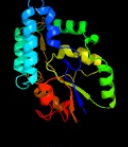





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1921c_(ppF)_2172531_2173802
Date	Fri Aug 2 13:30:54 BST 2019
Unique Job ID	9d2a1cdfa0e433d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4gxtA_</a>	 Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> a conserved functionally unknown protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown protein from2 anaerococcus prevotii dsm 20548
2	<a href="#">c4as2D_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> phosphorylcholine phosphatase; <b>PDBTitle:</b> pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
3	<a href="#">c3fvvA_</a>	 Alignment		99.5	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 bordetella pertussis tohama i
4	<a href="#">d2vkqa1</a>	 Alignment		99.4	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
5	<a href="#">d2bdua1</a>	 Alignment		99.4	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Pyrimidine 5'-nucleotidase (UMPH-1)
6	<a href="#">c3p96A_</a>	 Alignment		99.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine phosphatase serb; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
7	<a href="#">c3m1yA_</a>	 Alignment		99.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine phosphatase (serb); <b>PDBTitle:</b> crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
8	<a href="#">c4ezeB_</a>	 Alignment		99.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of had family hydrolase t0658 from salmonella2 enterica subsp. enterica serovar typhi (target efi-501419)
9	<a href="#">d2feaa1</a>	 Alignment		99.1	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> MtnX-like
10	<a href="#">d1j97a_</a>	 Alignment		99.1	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
11	<a href="#">c4nwiB_</a>	 Alignment		99.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> 7-methylguanosine phosphate-specific 5'-nucleotidase; <b>PDBTitle:</b> crystal structure of cytosolic 5'-nucleotidase iiib (cn-iiib) bound to2 cytidine

12	<a href="#">c4b6jA_</a>	Alignment		98.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine phosphatase; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase from t.2 onnurineus
13	<a href="#">c1y8aA_</a>	Alignment		98.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein af1437; <b>PDBTitle:</b> structure of gene product af1437 from archaeoglobus fulgidus
14	<a href="#">d1nnla_</a>	Alignment		98.6	24	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphoserine phosphatase
15	<a href="#">c3n28A_</a>	Alignment		98.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine phosphatase; <b>PDBTitle:</b> crystal structure of probable phosphoserine phosphatase from vibrio2 cholerae, unliganded form
16	<a href="#">d1rkua_</a>	Alignment		98.6	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Homoserine kinase ThrH
17	<a href="#">c3kd3A_</a>	Alignment		98.5	17	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoserine phosphohydrolase-like protein; <b>PDBTitle:</b> crystal structure of a phosphoserine phosphohydrolase-like protein2 from francisella tularensis subsp. tularensis schu s4
18	<a href="#">d1zs9a1</a>	Alignment		98.3	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Enolase-phosphatase E1
19	<a href="#">d1y8aa1</a>	Alignment		98.2	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> AF1437-like
20	<a href="#">c3mc1A_</a>	Alignment		98.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> predicted phosphatase, had family; <b>PDBTitle:</b> crystal structure of a predicted phosphatase from2 clostridium acetobutylicum
21	<a href="#">c3iruA_</a>	Alignment	not modelled	98.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> phosphonoacetaldehyde hydrolase like protein; <b>PDBTitle:</b> crystal structure of phosphonoacetaldehyde hydrolase like protein from2 oleispira antarctica
22	<a href="#">c3d6jA_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 from bacteroides fragilis
23	<a href="#">d1swva_</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like
24	<a href="#">d2hsza1</a>	Alignment	not modelled	97.8	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
25	<a href="#">c4umfC_</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase kdsc; <b>PDBTitle:</b> crystal structure of 3-deoxy-d-manno-octulosonate 8-2 phosphate phosphatase from moraxella catarrhalis in3 complex with magnesium ion, phosphate ion and kdo molecule
26	<a href="#">d1zrna_</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
27	<a href="#">c3nuqA_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative nucleotide phosphatase; <b>PDBTitle:</b> structure of a putative nucleotide phosphatase from saccharomyces2 cerevisiae
						<b>PDB header:</b> hydrolase

28	<a href="#">c3s6jC_</a>	Alignment	not modelled	97.7	19	<b>Chain:</b> C: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> the crystal structure of a hydrolase from pseudomonas syringae
29	<a href="#">c6f2xA_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein tyrosine kinase a; <b>PDBTitle:</b> structural characterization of the mycobacterium tuberculosis protein2 tyrosine kinase a (ptka)
30	<a href="#">c2yy6B_</a>	Alignment	not modelled	97.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of the phosphoglycolate phosphatase from aquifex2 aeolicus vf5
31	<a href="#">c3qypB_</a>	Alignment	not modelled	97.5	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> inorganic pyrophosphatase; <b>PDBTitle:</b> crystal structure of pyrophosphatase from bacteroides2 thetaiotaomicron, glu47asn mutant complexed with calcium and3 phosphate
32	<a href="#">c3sd7A_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphatase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of putative phosphatase from2 clostridium difficile
33	<a href="#">d1te2a_</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
34	<a href="#">c2p9jH_</a>	Alignment	not modelled	97.5	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> hypothetical protein aq2171; <b>PDBTitle:</b> crystal structure of aq2171 from aquifex aeolicus
35	<a href="#">d1wpga2</a>	Alignment	not modelled	97.5	9	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
36	<a href="#">c3um9A_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase, type ii; <b>PDBTitle:</b> crystal structure of the defluorinating l-2-haloacid dehalogenase2 bpro0530
37	<a href="#">d1zd3a1</a>	Alignment	not modelled	97.4	16	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
38	<a href="#">c2pibA_</a>	Alignment	not modelled	97.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated carbohydrates phosphatase tm_1254; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 thermotoga maritima
39	<a href="#">c4uasA_</a>	Alignment	not modelled	97.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein cbby; <b>PDBTitle:</b> crystal structure of cbby from rhodobacter sphaeroides in complex with2 phosphate
40	<a href="#">c3m9lA_</a>	Alignment	not modelled	97.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like family; <b>PDBTitle:</b> crystal structure of probable had family hydrolase from pseudomonas2 fluorescens pf-5
41	<a href="#">d2ah5a1</a>	Alignment	not modelled	97.3	20	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
42	<a href="#">c4hgnB_</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-d-manno-octulosonate 8-phosphate <b>PDBTitle:</b> crystal structure of 2-keto-3-deoxyoctulosonate 8-phosphate2 phosphohydrolase from bacteroides thetaiotaomicron
43	<a href="#">c2r8zC_</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of yrbi phosphatase from escherichia coli in complex2 with a phosphate and a calcium ion
44	<a href="#">c4uw9A_</a>	Alignment	not modelled	97.3	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> the crystal structural of archaean beta-phosphoglucomutase2 from hyper-thermophilic pyrococcus sp. strain st 04
45	<a href="#">d2b82a1</a>	Alignment	not modelled	97.3	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Class B acid phosphatase, AphA
46	<a href="#">c3umcC_</a>	Alignment	not modelled	97.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> haloacid dehalogenase; <b>PDBTitle:</b> crystal structure of the l-2-haloacid dehalogenase pa0810
47	<a href="#">c3mmzA_</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative had family hydrolase; <b>PDBTitle:</b> crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
48	<a href="#">c3niwA_</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase from2 bacteroides thetaiotaomicron
49	<a href="#">c3n07B_</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-deoxy-d-manno-octulosonate 8-phosphate phosphatase; <b>PDBTitle:</b> structure of putative 3-deoxy-d-manno-octulosonate 8-phosphate2 phosphatase from vibrio cholerae
50	<a href="#">c3mn1B_</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable yrbi family phosphatase; <b>PDBTitle:</b> crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
51	<a href="#">d1qyia_</a>	Alignment	not modelled	97.1	17	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Hypothetical protein MW1667 (SA1546)
52	<a href="#">c1zoxA_</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> phfad1;

52	<a href="#">c4e6A_</a>	Alignment	not modelled	97.1	14	<b>PDBTitle:</b> crystal structure of pfhad1 in complex with glyceraldehyde-3-phosphate <b>PDB header:</b> hydrolase
53	<a href="#">c4ex7A_</a>	Alignment	not modelled	97.1	19	<b>Chain:</b> A; <b>PDB Molecule:</b> alnb; <b>PDBTitle:</b> crystal structure of the alnumycin p phosphatase in complex with free2 phosphate
54	<a href="#">d2go7a1</a>	Alignment	not modelled	97.1	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
55	<a href="#">d1z5ga1</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Class B acid phosphatase, AphA
56	<a href="#">c3e8mD_</a>	Alignment	not modelled	97.1	24	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> acylneuraminate cytidylyltransferase; <b>PDBTitle:</b> structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
57	<a href="#">c3dv9A_</a>	Alignment	not modelled	97.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> putative beta-phosphoglucomutase from bacteroides vulgatus.
58	<a href="#">c2p11A_</a>	Alignment	not modelled	97.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative haloacid dehalogenase-like hydrolase2 (bx_e_b1342) from burkholderia xenovorans lb400 at 2.20 a resolution
59	<a href="#">c4fypA_</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> plant protein <b>Chain:</b> A; <b>PDB Molecule:</b> vegetative storage protein 1; <b>PDBTitle:</b> crystal structure of plant vegetative storage protein
60	<a href="#">d1k1ea_</a>	Alignment	not modelled	97.0	22	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Probable phosphatase YrbI
61	<a href="#">c3l5kA_</a>	Alignment	not modelled	97.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain-containing <b>PDBTitle:</b> the crystal structure of human haloacid dehalogenase-like hydrolase2 domain containing 1a (hdhd1a)
62	<a href="#">c2i34B_</a>	Alignment	not modelled	97.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> acid phosphatase; <b>PDBTitle:</b> the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
63	<a href="#">c4eekA_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-phosphoglucomutase-related protein; <b>PDBTitle:</b> crystal structure of had family hydrolase dr_1622 from deinococcus2 radiodurans r1 (target efi-501256) with bound phosphate and sodium
64	<a href="#">d2b8ea1</a>	Alignment	not modelled	96.9	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Meta-cation ATPase, catalytic domain P
65	<a href="#">c3umbA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of the l-2-haloacid dehalogenase rsc1362
66	<a href="#">c2hoqA_</a>	Alignment	not modelled	96.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative had-hydrolase ph1655; <b>PDBTitle:</b> crystal structure of the probable haloacid dehalogenase (ph1655) from2 pyrococcus horikoshii ot3
67	<a href="#">c4navB_</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> hypothetical protein xcc279; <b>PDBTitle:</b> crystal structure of hypothetical protein xcc2798 from xanthomonas2 campestris, target efi-508608
68	<a href="#">c2om6A_</a>	Alignment	not modelled	96.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> probable phosphoserine phosphatase; <b>PDBTitle:</b> hypothetical protein (probable phosphoserine phosph (ph0253) from2 pyrococcus horikoshii ot3
69	<a href="#">c3n1uA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hydrolase, had superfamily, subfamily iii a; <b>PDBTitle:</b> structure of putative had superfamily (subfamily iii a) hydrolase from2 legionella pneumophila
70	<a href="#">c2no5B_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> (s)-2-haloacid dehalogenase iva; <b>PDBTitle:</b> crystal structure analysis of a dehalogenase with intermediate complex
71	<a href="#">c2hi0B_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> putative phosphoglycolate phosphatase; <b>PDBTitle:</b> crystal structure of putative phosphoglycolate phosphatase2 (yp_619066.1) from lactobacillus delbrueckii subsp. bulgaricus atcc3 baa-365 at 1.51 a resolution
72	<a href="#">c3e58A_</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> putative beta-phosphoglucomutase; <b>PDBTitle:</b> crystal structure of putative beta-phosphoglucomutase from2 streptococcus thermophilus
73	<a href="#">d1qq5a_</a>	Alignment	not modelled	96.6	12	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> HAD-related
74	<a href="#">d2hcfa1</a>	Alignment	not modelled	96.6	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
75	<a href="#">c4rn3B_</a>	Alignment	not modelled	96.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> had superfamily hydrolase; <b>PDBTitle:</b> crystal structure of a had-superfamily hydrolase, subfamily ia,2 variant 1 (gsu2069) from geobacter sulfurreducens pca at 2.15 a3 resolution
76	<a href="#">c2qltA_</a>	Alignment	not modelled	96.5	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> (dl)-glycerol-3-phosphatase 1; <b>PDBTitle:</b> crystal structure of an isoform of dl-glycerol-3-phosphatase, rhr2p,2 from saccharomyces cerevisiae <b>PDB header:</b> hydrolase

77	<a href="#">c3r4cA</a>	Alignment	not modelled	96.5	14	<b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
78	<a href="#">c3skyA</a>	Alignment	not modelled	96.4	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase b; <b>PDBTitle:</b> 2.1a crystal structure of the phosphate bound atp binding domain of2 archaeoglobus fulgidus copb
79	<a href="#">c3fzqA</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydrolase; <b>PDBTitle:</b> crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
80	<a href="#">c3dnpA</a>	Alignment	not modelled	96.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> stress response protein yhax; <b>PDBTitle:</b> crystal structure of stress response protein yhax from bacillus2 subtilis
81	<a href="#">c3pgvB</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase; <b>PDBTitle:</b> crystal structure of a haloacid dehalogenase-like hydrolase2 (kpn_04322) from klebsiella pneumoniae subsp. pneumoniae mgh 78578 at3 2.39 a resolution
82	<a href="#">d2hdoa1</a>	Alignment	not modelled	96.4	19	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
83	<a href="#">c3i28A</a>	Alignment	not modelled	96.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxide hydrolase 2; <b>PDBTitle:</b> crystal structure of soluble epoxide hydrolase
84	<a href="#">c3rfuC</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> copper efflux atpase; <b>PDBTitle:</b> crystal structure of a copper-transporting pib-type atpase
85	<a href="#">c2qyH_D</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical conserved protein, gk1056; <b>PDBTitle:</b> crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
86	<a href="#">c3j08A</a>	Alignment	not modelled	96.3	23	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
87	<a href="#">d1nrwa</a>	Alignment	not modelled	96.3	18	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
88	<a href="#">c3et4A</a>	Alignment	not modelled	96.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein p4, nadp phosphatase; <b>PDBTitle:</b> structure of recombinant haemophilus influenzae e(p4) acid phosphatase
89	<a href="#">c5mrwF</a>	Alignment	not modelled	96.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> potassium-transporting atpase atp-binding subunit; <b>PDBTitle:</b> structure of the kdpfabc complex
90	<a href="#">c3ewiB</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acylneuraminate cytidylyltransferase; <b>PDBTitle:</b> structural analysis of the c-terminal domain of murine cmp-sialic acid2 synthetase
91	<a href="#">d2b0ca1</a>	Alignment	not modelled	96.2	13	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> YihX-like
92	<a href="#">c2b8eB</a>	Alignment	not modelled	96.2	20	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation-transporting atpase; <b>PDBTitle:</b> copa atp binding domain
93	<a href="#">c2odaB</a>	Alignment	not modelled	96.1	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein pspto_2114; <b>PDBTitle:</b> crystal structure of pspto_2114
94	<a href="#">c4uavA</a>	Alignment	not modelled	96.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase-like hydrolase domain-containing <b>PDBTitle:</b> crystal structure of cbby (at3g48420) from arabidopsis thaliana
95	<a href="#">c3daoB</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphate; <b>PDBTitle:</b> crystal structure of a putative phosphate (eubrec_1417) from2 eubacterium rectale at 1.80 a resolution
96	<a href="#">c3cnhA</a>	Alignment	not modelled	96.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase family protein; <b>PDBTitle:</b> crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
97	<a href="#">c3pctA</a>	Alignment	not modelled	96.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> class c acid phosphatase; <b>PDBTitle:</b> structure of the class c acid phosphatase from pasteurella multocida
98	<a href="#">c4gibA</a>	Alignment	not modelled	96.0	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> 2.27 angstrom crystal structure of beta-phosphoglucomutase (pgmb) from2 clostridium difficile
99	<a href="#">c3j09A</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> hydrolase, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> copper-exporting p-type atpase a; <b>PDBTitle:</b> high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa
100	<a href="#">d2rbka1</a>	Alignment	not modelled	96.0	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
101	<a href="#">d2fi1a1</a>	Alignment	not modelled	96.0	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Phosphonoacetaldehyde hydrolase-like

102	<a href="#">c2pkeA_</a>	Alignment	not modelled	95.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid delahogenase-like family hydrolase; <b>PDBTitle:</b> crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
103	<a href="#">c1mhsA_</a>	Alignment	not modelled	95.9	14	<b>PDB header:</b> membrane protein, proton transport <b>Chain:</b> A: <b>PDB Molecule:</b> plasma membrane atpase; <b>PDBTitle:</b> model of neurospora crassa proton atpase
104	<a href="#">c2iyeC_</a>	Alignment	not modelled	95.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> copper-transporting atpase; <b>PDBTitle:</b> structure of catalytic cpx-atpase domain copb-b
105	<a href="#">d2fdra1</a>	Alignment	not modelled	95.7	14	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> beta-Phosphoglucomutase-like
106	<a href="#">d1rkqa_</a>	Alignment	not modelled	95.6	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
107	<a href="#">c2ympB_</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> l-haloacid dehalogenase; <b>PDBTitle:</b> chloroacetic acid complex bound l-haloacid dehalogenase2 from a rhodobacteraceae family bacterium
108	<a href="#">d1q92a_</a>	Alignment	not modelled	95.4	9	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> 5'(3')-deoxyribonucleotidase (dNT-2)
109	<a href="#">c3ddhA_</a>	Alignment	not modelled	95.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative haloacid dehalogenase-like family hydrolase; <b>PDBTitle:</b> the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482
110	<a href="#">c4umwA_</a>	Alignment	not modelled	95.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc-transporting atpase; <b>PDBTitle:</b> crystal structure of a zinc-transporting pib-type atpase in2 e2.pi state
111	<a href="#">c3nasA_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-phosphoglucomutase; <b>PDBTitle:</b> the crystal structure of beta-phosphoglucomutase from bacillus2 subtilis
112	<a href="#">c6roiA_</a>	Alignment	not modelled	95.3	25	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> probable phospholipid-transporting atpase drs2; <b>PDBTitle:</b> cryo-em structure of the partially activated drs2p-cdc50p
113	<a href="#">c3b8cB_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase 2, plasma membrane-type; <b>PDBTitle:</b> crystal structure of a plasma membrane proton pump
114	<a href="#">c3b9bA_</a>	Alignment	not modelled	95.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcoplasmic/endoplasmic reticulum calcium <b>PDBTitle:</b> structure of the e2 beryllium fluoride complex of the serca2 ca2+-atpase
115	<a href="#">d1xvia_</a>	Alignment	not modelled	95.2	21	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
116	<a href="#">c1xviA_</a>	Alignment	not modelled	95.2	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative mannosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
117	<a href="#">c2i7dB_</a>	Alignment	not modelled	95.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 5'(3')-deoxyribonucleotidase, cytosolic type; <b>PDBTitle:</b> structure of human cytosolic deoxyribonucleotidase in2 complex with deoxyridine, alf4 and mg2+
118	<a href="#">c2pr7A_</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> haloacid dehalogenase/epoxide hydrolase family; <b>PDBTitle:</b> crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
119	<a href="#">d1wzca1</a>	Alignment	not modelled	95.0	15	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof
120	<a href="#">d1wr8a_</a>	Alignment	not modelled	94.9	11	<b>Fold:</b> HAD-like <b>Superfamily:</b> HAD-like <b>Family:</b> Predicted hydrolases Cof